

Draper

1646

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/920,608

DATE: 02/11/1999
TIME: 15:29:53

INPUT SET: S30598.raw

pt#12

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: Pelleymounter, Mary Ann
Hecht, Randy I
Mann, Michael B

(ii) TITLE OF INVENTION: OB PROTEIN COMPOSITIONS AND METHODS

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Amgen Inc.
(B) STREET: 1840 Dehavilland Drive
(C) CITY: Thousand Oaks
(D) STATE: California
(E) COUNTRY: U.S.A.
(F) ZIP: 91230-1789

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/474,833
(B) FILING DATE: 07-JUN-1995
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Pessin, Karol M.
(C) REFERENCE/DOCKET NUMBER: A-345

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 491 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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PATENT APPLICATION US/08/920,608DATE: 02/11/1999
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INPUT SET: S30598.raw

47
48
49
50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
51
52 TCTAGATTTG AGTTTTAACT TTTAGAAGGA GGAATAACAT ATGGTACCGA TCCAGAAAGT 60
53
54 TCAGGACGAC ACCAAAACCT TAATTAAAAC GATCGTTACG CGTATCAACG ACATCAGTCA 120
55
56 CACCCAGTCG GTCTCCGCTA AACAGCGTGT TACCGGTCTG GACTTCATCC CGGGTCTGCA 180
57
58 CCCGATCCTA AGCTTGTCCA AAATGGACCA GACCCTGGCT GTATACCAGC AGGTGTTAAC 240
59
60 CTCCCTGCCG TCCCAGAACG TTCTTCAGAT CGCTAACGAC CTCGAGAACC TTCGCGACCT 300
61
62 GCTGCACCTG CTGGCATTCT CCAAATCCTG CTCCCTGCCG CAGACCTCAG GTCTTCAGAA 360
63
64 ACCGGAATCC CTGGACGGGG TCCTGGAAGC ATCCCTGTAC AGCACCGAAG TTGTTGCTCT 420
65
66 GTCCCGTCTG CAGGGTTCCT TTCAGGACAT CCTTCAGCAG CTGGACGTTT CTCCGGAATG 480
67
68 TTAATGGATC C 491

69
70 (2) INFORMATION FOR SEQ ID NO:2:
71

72 (i) SEQUENCE CHARACTERISTICS:
73 (A) LENGTH: 491 base pairs
74 (B) TYPE: nucleic acid
75 (C) STRANDEDNESS: double
76 (D) TOPOLOGY: linear
77

78 (ii) MOLECULE TYPE: cDNA
79
80
81
82

83 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
84

85 AGATCTAAAC TCAAAATTGA AAATCTTCCT CCTTATTGTA TACCATGGCT AGGTCTTTCA 60
86
87 AGTCCTGCTG TGGTTTTGGA ATTAATTTTG CTAGCAATGC GCATAGTTGC TGTAAGTCAGT 120
88
89 GTGGGTCAGC CAGAGGCGAT TTGTCGCACA ATGGCCAGAC CTGAAGTAGG GCCCAGACGT 180
90
91 GGGCTAGGAT TCGAACAGGT TTTACCTGGT CTGGGACCGA CATATGGTCG TCCACAATTG 240
92
93 GAGGGACGGC AGGGTCTTGC AAGAAGTCTA GCGATTGCTG GAGCTCTTGG AAGCGCTGGA 300
94
95 CGACGTGGAC GACCGTAAGA GGTTTAGGAC GAGGGACGGC GTCTGGAGTC CAGAAGTCTT 360
96
97 TGGCCTTAGG GACCTGCCCC AGGACCTTCG TAGGGACATG TCGTGGCTTC AACACGAGA 420
98
99 CAGGGCAGAC GTCCCAAGGG AAGTCCTGTA GGAAGTCGTC GACCTGCAAA GAGGCCTTAC 480

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/920,608DATE: 02/11/1999
TIME: 15:29:54

INPUT SET: S30598.raw

100
101 AATTACCTAG G 491
102
103 (2) INFORMATION FOR SEQ ID NO:3:
104
105 (i) SEQUENCE CHARACTERISTICS:
106 (A) LENGTH: 147 amino acids
107 (B) TYPE: amino acid
108 (C) STRANDEDNESS: single
109 (D) TOPOLOGY: linear
110
111 (ii) MOLECULE TYPE: protein
112
113
114
115
116 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
117
118 Met Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys
119 1 5 10 15
120
121 Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser
122 20 25 30
123
124 Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro
125 35 40 45
126
127 Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln
128 50 55 60
129
130 Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln Ile Ala Asn Asp
131 65 70 75 80
132
133 Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala Phe Ser Lys Ser
134 85 90 95
135
136 Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro Glu Ser Leu Asp
137 100 105 110
138
139 Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val Ala Leu Ser
140 115 120 125
141
142 Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln Leu Asp Val Ser
143 130 135 140
144
145 Pro Glu Cys
146 145
147
148 (2) INFORMATION FOR SEQ ID NO:4:
149
150 (i) SEQUENCE CHARACTERISTICS:
151 (A) LENGTH: 454 base pairs
152 (B) TYPE: nucleic acid

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/920,608DATE: 02/11/1999
TIME: 15:29:54

INPUT SET: S30598.raw

153 (C) STRANDEDNESS: double
154 (D) TOPOLOGY: linear
155

156 (ii) MOLECULE TYPE: cDNA
157
158
159
160

161 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
162

163	CATATGGTAC CGATCCAGAA AGTTCAGGAC GACACCAAAA CCTTAATTAA AACGATCGTT	60
164		
165	ACGCGTATCA ACGACATCAG TCACACCCAG TCGGTGAGCT CTAAACAGCG TGTTACAGGC	120
166		
167	CTGGACTTCA TCCCGGGTCT GCACCCGATC CTGACCTTGT CCAAATGGA CCAGACCCTG	180
168		
169	GCTGTATACC AGCAGATCTT AACCTCCATG CCGTCCCGTA ACGTTCTTCA GATCTCTAAC	240
170		
171	GACCTCGAGA ACCTTCGCGA CCTGCTGCAC GTGCTGGCAT TCTCCAAATC CTGCCACCTG	300
172		
173	CCATGGGCTT CAGGTCTTGA GACTCTGGAC TCTCTGGGCG GGGTCCTGGA AGCATCCGGT	360
174		
175	TACAGCACCG AAGTTGTTGC TCTGTCCCGT CTGCAGGGTT CCCTTCAGGA CATGCTTTGG	420
176		
177	CAGCTGGACC TGTCTCCGGG TTGTTAATGG ATCC	454
178		

179 (2) INFORMATION FOR SEQ ID NO:5:
180

181 (i) SEQUENCE CHARACTERISTICS:
182 (A) LENGTH: 454 base pairs
183 (B) TYPE: nucleic acid
184 (C) STRANDEDNESS: double
185 (D) TOPOLOGY: linear
186

187 (ii) MOLECULE TYPE: cDNA
188
189
190
191

192 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
193

194	GTATACCATG GCTAGGTCTT TCAAGTCCTG CTGTGGTTTT GGAATTAATT TTGCTAGCAA	60
195		
196	TGCGCATAGT TGCTGTAGTC AGTGTGGGTC AGCCACTCGA GATTTGTCGC ACAATGTCCG	120
197		
198	GACCTGAAGT AGGGCCCAGA CGTGGGCTAG GACTGGAACA GGTTTTACCT GGTCTGGGAC	180
199		
200	CGACATATGG TCGTCTAGAA TTGGAGGTAC GGCAGGGCAT TGCAAGAAGT CTAGAGATTG	240
201		
202	CTGGAGCTCT TGGAAGCGCT GGACGACGTG CACGACCGTA AGAGGTTTAG GACGGTGGAC	300
203		
204	GGTACCCGAA GTCCAGAACT CTGAGACCTG AGAGACCCGC CCCAGGACCT TCGTAGGCCA	360
205		

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/920,608DATE: 02/11/1999
TIME: 15:29:55

INPUT SET: S30598.raw

206 ATGTCGTGGC TTCAACAACG AGACAGGGCA GACGTCCCAA GGGAAGTCCT GTACGAAACC 420

207

208 GTCGACCTGG ACAGAGGCCC AACAATTACC TAGG 454

209

210 (2) INFORMATION FOR SEQ ID NO:6:

211

212 (i) SEQUENCE CHARACTERISTICS:

213 (A) LENGTH: 147 amino acids

214 (B) TYPE: amino acid

215 (C) STRANDEDNESS: single

216 (D) TOPOLOGY: linear

217

218 (ii) MOLECULE TYPE: protein

219

220

221

222

223 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

224

225 Met Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys
226 1 5 10 15

227

228 Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser
229 20 25 30

230

231 Ser Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro
232 35 40 45

233

234 Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln
235 50 55 60

236

237 Ile Leu Thr Ser Met Pro Ser Arg Asn Val Leu Gln Ile Ser Asn Asp
238 65 70 75 80

239

240 Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser Lys Ser
241 85 90 95

242

243 Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu Gly
244 100 105 110

245

246 Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu Ser
247 115 120 125

248

249 Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu Ser
250 130 135 140

PAGE: 1

SEQUENCE VERIFICATION REPORT
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Line	Error	Original Text
28	Wrong application Serial Number	(A) APPLICATION NUMBER: US 08/474,833